PhytoKeys 266: 241–252 (2025)
DOI: 10.3897/phytokeys.266.147400

Research Article

# *Balanophora xinfeniae* (Balanophoraceae), a new species from Xizang, China

Chen-Long Fu[1], Jia-Ning Zhou[1], Wei-Hua Liao[1], Tong Zhang[2], Bo Xu[3], Meng Li[1]

1 *Co-Innovation Center for the Sustainable Forestry in Southern China, College of life sciences, Nanjing Forestry University, Nanjing 210037, Jiangsu, China*
2 *Central South Inventory and Planning Institute of National Forestry and Grassland Administration, Changsha, 410014, China*
3 *CAS Key Laboratory of Mountain Ecological Restoration and Bioresource Utilization & Ecological Restoration and Biodiversity Conservation Key Laboratory of Sichuan Province, Chengdu Institute of Biology, Chinese Academy of Sciences, Chengdu 610213, Sichuan, China*

*Corresponding authors: Bo Xu (xubo@cib.ac.cn); Meng Li (limeng@njfu.edu.cn)*

## Abstract

*Balanophora xinfeniae* C.L.Fu, M.Li & B.Xu, a new species discovered in Xizang, China, is described and illustrated here. Molecular phylogenetic analyses and morphological comparisons strongly support *B. xinfeniae* as a new species within the genus *Balanophora*. The most distinctive characteristic of the new species is its dioecious sexual system, with male flowers having a 3-lobed perianth, opposite leaves with serrated tips, and yellow scapes. Although it shares morphological similarities with *B. henryi*, *B. xinfeniae* can be distinguished by its flat spheroid tubers without stellate lenticels, yellow scape, prominently serrated apical leaf margins, and nearly spherical or ovoid-ellipsoid female inflorescences.

**Key words:** *Balanophora xinfeniae*, China, holoparasitic plants, phylogeny, taxonomy

OPEN ACCESS

Academic editor:
Marcos A. Caraballo-Ortiz
**Received:** 1 January 2025
**Accepted:** 5 November 2025
**Published:** 19 November 2025

**Citation:** Fu C-L, Zhou J-N, Liao W-H, Zhang T, Xu B, Li M (2025) *Balanophora xinfeniae* (Balanophoraceae), a new species from Xizang, China. PhytoKeys 266: 241–252. https://doi.org/10.3897/phytokeys.266.147400

**Copyright:** © Chen-Long Fu et al.
This is an open access article distributed under terms of the Creative Commons Attribution License (Attribution 4.0 International – CC BY 4.0).

## Introduction

*Balanophora* J. R. Forst. & G. Forst. is a genus of holoparasitic plants consisting of about 25 species distributed mainly in tropical Southeast and East Asia (Hansen 1972; Mutinda et al. 2024). In traditional medicine, species of *Balanophora* are often used to treat hemorrhoids, stomach aches, and liver ailments and can also be used as antipyretics (Teng et al. 2000; Li et al. 2006; Trakulsomboon et al. 2006; Mutinda et al. 2024). Regarding their lifestyle, *Balanophora* comprises highly specialized root holoparasites characterized by underground connections with their hosts. Over an extended period of adaptive evolution, these plants have experienced significant gene loss from their genomes (Su et al. 2019; Chen et al. 2023) and extensive morphological reduction, leaving only a limited number of traits available for taxonomic classification (Job and Bertel 2015; Yu et al. 2022).

Morphologically, *Balanophora* can be readily divided into two subgenera: subgenus *Balanophora* (4- to 6-merous male flowers) and subgenus *Balania* (3-merous male flowers), a result that is also supported by molecular systematics (Yu et al. 2022). However, resolving relationships among these subgenera at the species level continues to be a challenging task. DNA regions with

high substitution rates provide effective tools to evaluate the monophyly of *Balanophora* species defined by morphological traits. Recent studies have improved our understanding of species boundaries within this genus by comparing classifications based on morphological characters with results from molecular phylogenetic analyses (Hsiao et al. 2010; Su et al. 2012; Yu et al. 2021). For instance, Hansen (1972) considered the morphological differences among several species as intraspecific variation, synonymizing them under *B. harlandii*. In contrast, a more recent study based primarily on molecular phylogenetic analysis provided support for recognizing three distinct taxa—*B. harlandii*, *B. henryi*, and *B. kawakamii*—with clades corresponding to these taxa being strongly supported by molecular data (Yu et al. 2022).

During our fieldwork from April to May 2024 in the forests near Gelin Village, Motuo County, Xizang (China), we discovered a *Balanophora* that differed from all previously described species reported in China, India, Nepal, and other countries. Through morphological observations and the construction of a phylogenetic tree using nuclear ribosomal internal transcribed spacer (ITS) sequences, we concluded that this taxon represents an undescribed species of *Balanophora*.

## Materials and methods

### Morphological study

Morphological observations were conducted based on living plants in the field. Measurements were performed manually with rulers in the field or with the software ImageJ in the laboratory using photographs. We restricted morphological comparisons to three closely related species. At the same time, all images of specimens potentially related to the new species from China, India, Nepal, and other countries deposited in the herbaria A, CDBI, CDCM, GAC, HHBG, IBSC, IBK, LBG, K, KUN, NAS, P, PE, SHM, and ZM were observed and studied (acronyms follow Thiers 2024). The terminology used in the morphological description follows the Flora of China (Huang and Murata 2003). Observations of flowers and claviform bodies were carried out using an Olympus SZX10 stereomicroscope.

### Phylogenetic study

DNA extractions, PCR procedures, and primers followed Yu et al. (2021). The ITS region of the new species was sequenced using the Sanger method. In addition, we downloaded ITS sequences of other *Balanophora* species available in the Nucleotide database of NCBI (https://www.ncbi.nlm.nih.gov). *Langsdorffia hypogaea* was selected as the outgroup for this study based on the results presented by Sanchez-Puerta et al. (2023). A total of 54 samples were used in this study, including multiple accessions for some species (Table 1). All sequences were aligned using MAFFT v7.526 following default parameters (Katoh et al. 2002; Katoh and Standley 2013), and the ends were manually trimmed. The model TPM3u+F+I+R2 for ML analysis and TPM3uf+I+G for BI analysis was selected based on the Bayesian Information Criterion (BIC) using jModelTest v2.1.10 (Darriba et al. 2012). Maximum likelihood (ML) analyses were performed using IQ-TREE v2.3.6 with 10,000 ultrafast bootstrap approximations (Minh et al. 2020). A Bayesian inference (BI) analysis was performed using

MrBayes v3.2.7 (Ronquist et al. 2012). A Markov chain Monte Carlo analysis was conducted for 20,000,000 generations with one cold and three hot chains, each starting from a random tree and sampled every 1,000 generations. The first 25% of the trees were discarded as burn-in, and the remaining trees were used to construct majority-rule consensus trees. The final trees obtained from the ML and BI analyses were visualized using FigTree v1.4.2 (Rambaut 2009).

## Results and discussion

The circumscription of *B. flava*, *B. fargesii*, and *B. involucrata* remains a persistent taxonomic contention. Geng (2016) proposed that *B. fargesii* and *B. involucrata* are sister groups with distinct clades based on ITS sequences. In contrast, Lidén (2019) suggested that *B. fargesii* is synonymous with *B. involucrata*, while Yu et al. (2022) posited that *B. flava* and *B. fargesii* are synonymous with *B. involucrata*. In this study, these species are considered part of the *B. involucrata* complex, and we are not addressing taxonomic divisions within this group here. Instead, for clarity and to facilitate morphological comparisons, we refer to the dioecious individuals within the complex as *B. flava* and the monoecious individuals as *B. involucrata*.

**Table 1.** Taxa used in the phylogenetic analyses with their GenBank accession numbers.

| Species | Accession number | Species | Accession number |
|---|---|---|---|
| *B. appressa* | MW414662 | *B. laxiflora* | JN392888 |
| *B. appressa* | MW414670 | *B. laxiflora* | JN392889 |
| *B. flava* | OM103570 | *B. laxiflora* | MW414661 |
| *B. flava* | OM103567 | *B. laxiflora* | MW414659 |
| *B. fungosa* | JN392881 | *B. laxiflora* | JN392890 |
| *B. harlandii* | OM103582 | *B. laxiflora* | JN392891 |
| *B. harlandii* | OM103583 | *B. laxiflora* | JN392892 |
| *B. harlandii* | OM103585 | *B. laxiflora* | JN392893 |
| *B. henryi* | OM103573 | *B. parajaponica* | MT482093 |
| *B. henryi* | OM103574 | *B. parajaponica* | MT498081 |
| *B. henryi* | OM103575 | *B. parajaponica* | MW414666 |
| *B. henryi* | OM103576 | *B. parajaponica* | MW414667 |
| *B. henryi* | OM103577 | *B. reflexa* | EU598798 |
| *B. indica* | JN392880 | *B. reflexa* | KT763380 |
| *B. involucrata* | OM103568 | *B. subcupularis* | OM103584 |
| *B. involucrata* | OM103569 | *B. subcupularis* | OM418783 |
| *B. involucrata* | OM103571 | *B. subcupularis* | OM418784 |
| *B. involucrata* | OM103572 | *B. tobiracola* | JN392901 |
| *B. japonica* | JN392882 | *B. tobiracola* | OM103578 |
| *B. japonica* | MW414664 | ***B. xinfeniae*** | **PQ640032** |
| *B. japonica* | MW414665 | ***B. xinfeniae*** | **PQ640033** |
| *B. kawakamii* | JN392900 | *B. yakushimensis* | JN392894 |
| *B. kawakamii* | OM103579 | *B. yakushimensis* | MW414660 |
| *B. kawakamii* | OM103580 | *B. yakushimensis* | MW414663 |
| *B. kawakamii* | OM103581 | *B. yakushimensis* | MW414668 |
| *B. latisepala* | OM418779 | *B. yakushimensis* | MW414669 |
| *B. latisepala* | OP120928 | *Langsdorffia hypogaea* | KT709672 |

The topologies of the phylogenetic trees constructed by the ML and BI methods are highly consistent (Suppl. materials 1, 2). Our results showed that two samples of the new species were well resolved as a distinct clade, which is the sister group to the *B. involucrata* complex (BS = 1; PP = 98%) (Fig. 1).

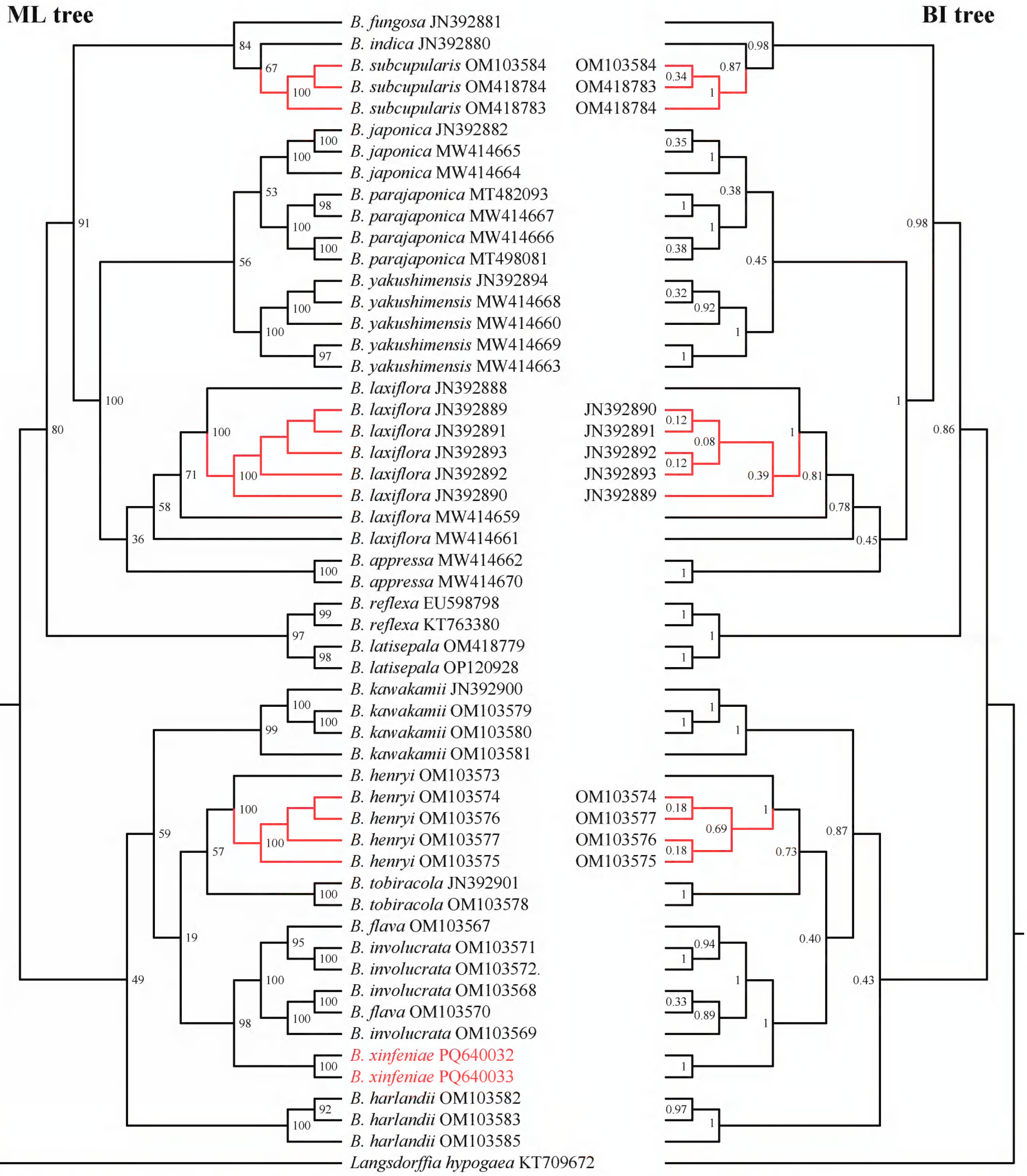


**Figure 1.** The cladogram of *Balanophora* constructed using maximum likelihood (left) and Bayesian inference (right) based on ITS sequences. Numbers at nodes indicate posterior probabilities (PP) or bootstrap percentages (BS). Branches highlighted in red indicate topological incongruence between the two trees. Labels for concordant topologies are not displayed on the BI tree.

The new species described in this study is morphologically most similar to *B. henryi*, along with the closely related species *B. involucrata* and *B. flava*. In the phylogeny, the new species was placed in a clade containing these three species (Fig. 1). We therefore focused our comparison of morphological characters on these four species (Table 2; Fig. 2). The most distinctive characteristics of the new species are its dioecious sexual system (vs. monoecious in *B. involucrata*), opposite leaves (vs. connate into a single sheath-like whorl in *B. flava* and *B. involucrata*) with serrated margins (vs. crenate in *B. flava* and *B. involucrata* and entire in *B. henryi*), and yellow scapes (vs. red in *B. involucrata* and red or red to yellow in *B. henryi*).

Based on the results of molecular and morphological analyses, we believe that there is sufficient evidence to support the validity of this taxon as distinctly different from *B. henryi*, *B. involucrata*, and *B. flava*. Therefore, we recommend that it be treated as a new species.

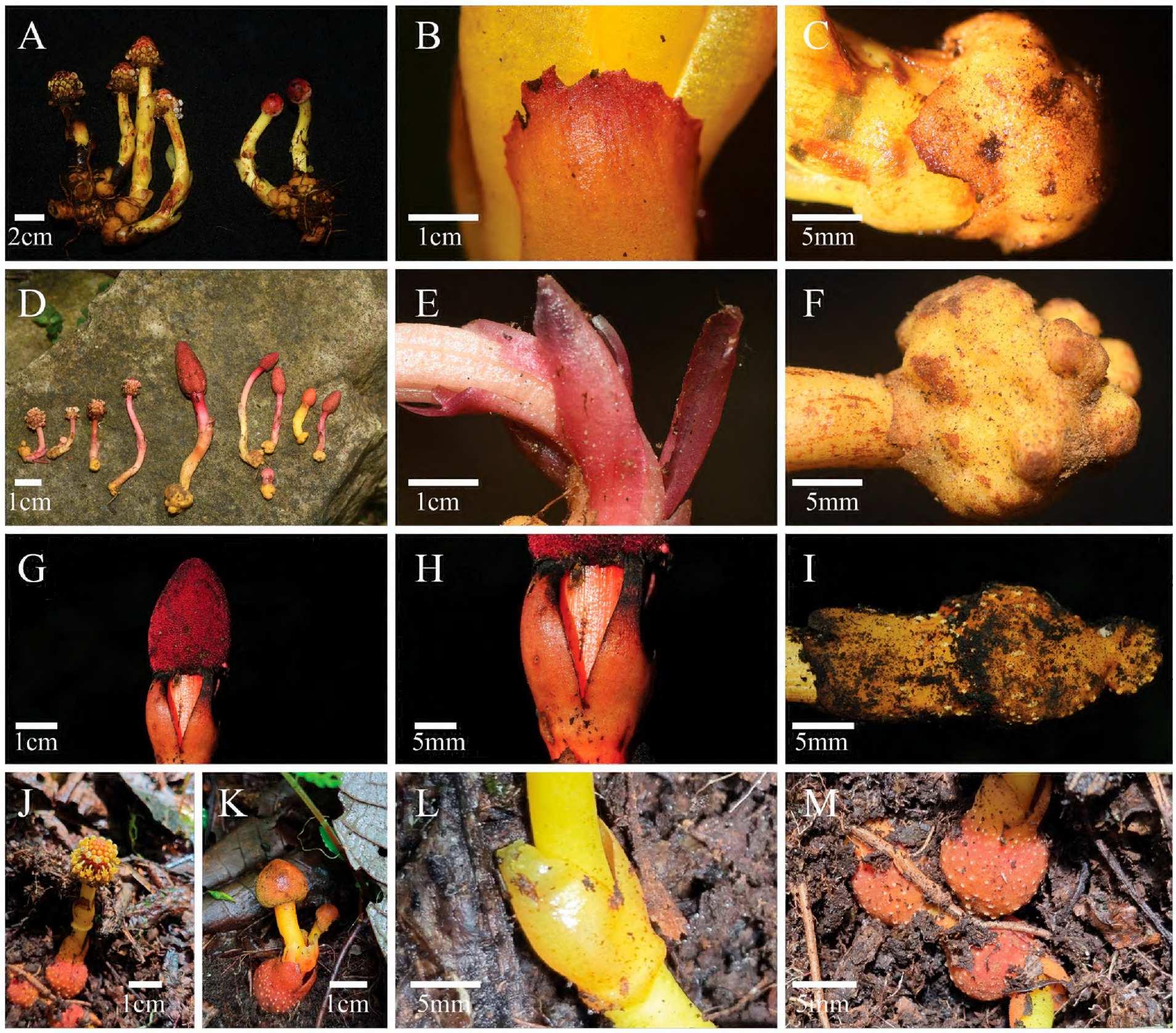


**Figure 2.** Morphology of *Balanophora xinfeniae* (**A–C**), *B. henryi* (**D–F**), *B. involucrata* (**G–I**), and *B. flava* (J–M). **A, D, G, J, K.** Male and female individuals; **B, E, H, L.** Leaves; **C, F, I, M.** Tubers. Photos by Meng Li and Wei-Hua Liao.

## Taxonomic treatment

***Balanophora xinfeniae* C.L.Fu, M.Li & B.Xu, sp. nov.**
urn:lsid:ipni.org:names:77372106-1
Figs 3, 4

**Type.** China • Xizang Autonomous Region: Motuo County (Mêdog), Gelin Village, 29.210161, 95.191856, alt. 1650 m, 29 Apr 2024 (fl.), *Meng Li, C.L. Fu & J.N. Zhou YLZB11691-A* (holotype: CDBI! Barcode number: CDBI0298364, ♀; isotypes: NAS! Barcode number: NAS00708465; NF!).

**Diagnosis.** *Balanophora xinfeniae* is morphologically similar to *B. henryi*, but the two species can be distinguished by several features. The tuber branching shape of *B. xinfeniae* is characterized as flat spheroid or subglobose, whereas that of *B. henryi* is irregularly spherical or oblate. The scapes of *B. xinfeniae* are yellow, in contrast to the red or red-to-yellow scapes of *B. henryi*. In *B. xinfeniae*, the apical margins of the leaves are prominently serrate, whereas those of *B. henryi* are entire. The female inflorescence of *B. xinfeniae* is nearly spherical or ovoid-ellipsoid, while that of *B. henryi* is broadly ovoid. The flowering period of *B. xinfeniae* is from April to May, compared to September to November for *B. henryi* (Table 2; Fig. 2).

**Description.** Plants dioecious. Tuber yellowish brown, branched or unbranched, surface scabrous, densely covered with granular warts; tuber branches flat spheroid or subglobose, 0.8–2.0 cm in diam. Scapes yellow, 2–12 × 0.5–1.2 cm. Leaves 6–10, yellow to reddish, opposite, scaly, oblong-ovate, apical margins prominently and irregularly serrate, with serrations arranged approximately parallel to the leaf margin, 1.2–3.5 × 0.3–1.8 cm. Male inflorescences subspheroid to ovoid-ellipsoid, 1.8–2.5 × 1.5–2.0 cm. Bracts truncate with expanded liplike margin, fused side by side into a hexagonal alveolus. Male flowers: pedicellate, inserted basally in alveolus, 3-merous, 2–4 mm in diam. Perianth lobes broadly deltoid. Synandria subdiscoid; anthers 3, transversely dehiscent. Female inflorescence nearly spherical or ovoid-ellipsoid. Claviform bodies obovoid, shortly stiped, apically truncate; cuticular ridges of apical cells labyrinth-like. Female flowers: both in the lower parts of the claviform bodies and on the main axis of the inflorescence.

**Table 2.** Comparison of morphological features among four related species of *Balanophora*.

| | ***B. xinfeniae*** | ***B. henryi*** | ***B. involucrata*** | ***B. flava*** |
|---|---|---|---|---|
| Reproduction | Dioecious | Dioecious | Monoecious | Dioecious |
| Tuber branching shape | Flat spheroid or subglobose | Irregularly spherical or oblate | Urceolate, slightly elongated | Urceolate |
| Tuber surface | Densely covered with granular warts | Densely covered with granular warts | Densely covered with granular warts and yellowish stellate lenticels | Densely covered with granular warts and yellowish stellate lenticels |
| Color of scapes | Yellow | Red or red to yellow | Red | Yellow |
| Leaf arrangement | Opposite | Opposite | Connate into a single sheath-like whorl | Connate into a single sheath-like whorl |
| Leaves apex | Serrated | Entire | Crenate | Crenate |
| Shape of female inflorescence | Nearly spherical or ovoid-ellipsoid | Broadly ovoid | Ovoid or short ellipsoid | Ovoid or short ellipsoid |
| Flowering period | April to May | September to November | July to August | July to August |

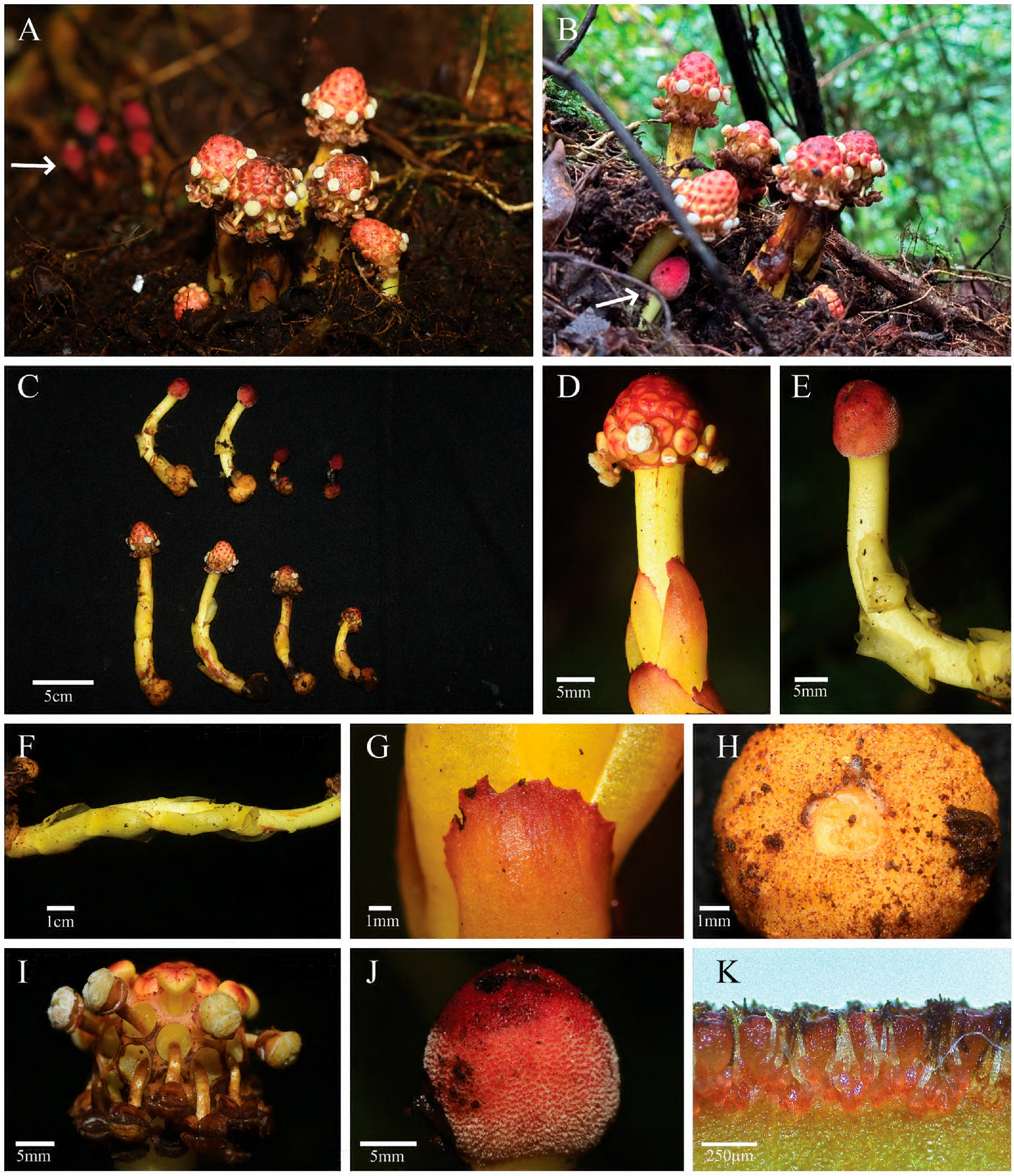


**Figure 3.** *Balanophora xinfeniae* C.L. Fu, M. Li & B. Xu. **A, B.** Habitats (both male and female; arrows point to female individuals); **C.** Female individual (upper) and male individual (lower); **D.** Male individual; **E.** Female individual; **F.** Leaves and scape; **G.** Leaves; **H.** Tuber; **I.** Male inflorescence; **J.** Female inflorescence; **K.** Female flower and claviform body. Photos by Meng Li and Chen-Long Fu.

**Distribution and habitat.** The new species is currently known only from the type locality in Gelin Village, Motuo County, Xizang Autonomous Region (Fig. 5). It grows in shaded forest habitats on moist mountain slopes. The hosts are usually species of Fagaceae, such as *Quercus lamellosa* and *Castanopsis indica*.

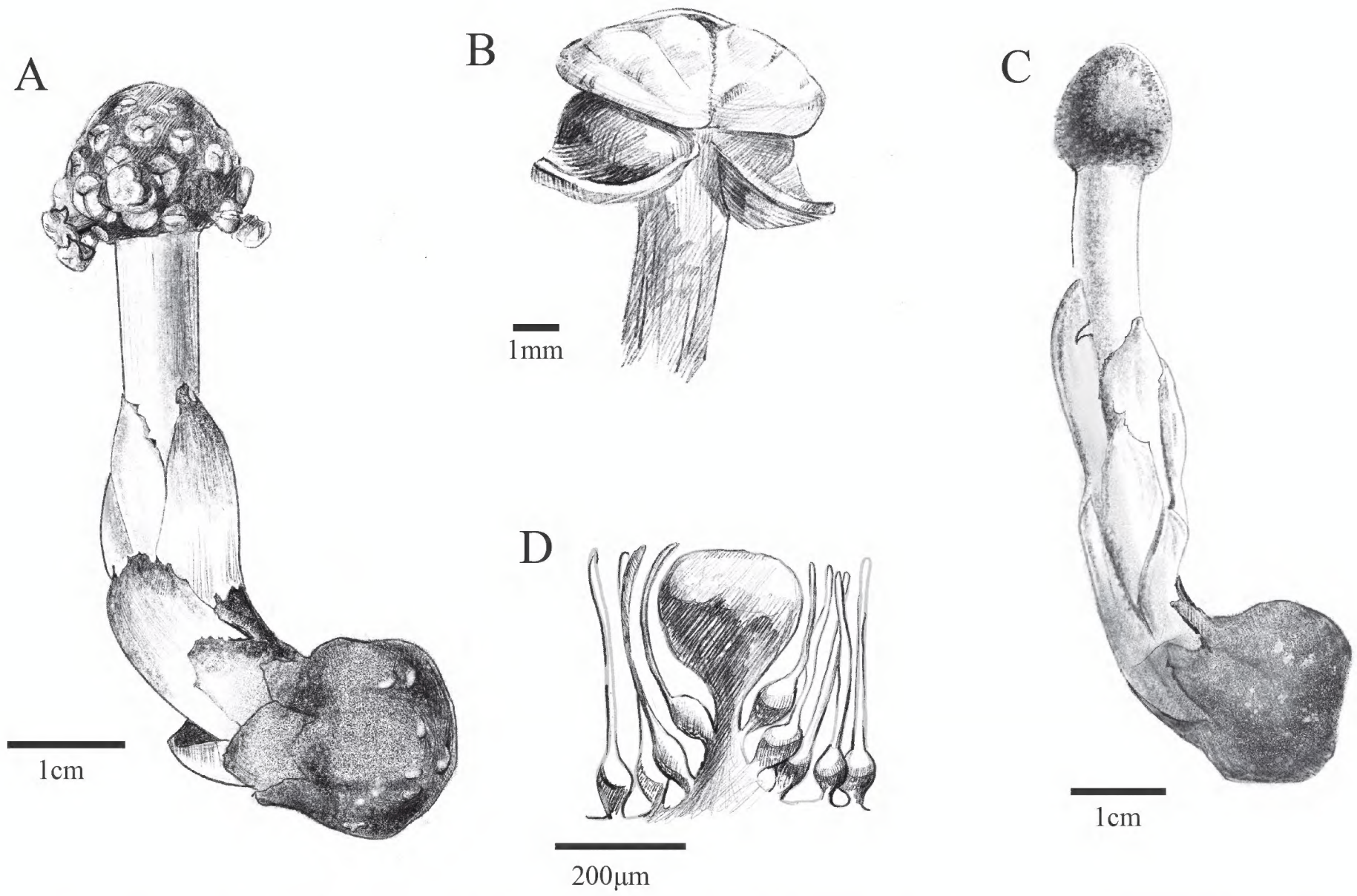


**Figure 4.** Line illustration of *Balanophora xinfeniae*. **A.** Male individual; **B.** Male flower; **C.** Female individual; **D.** Female flowers surrounding one claviform body. Drawn by Zi-Heng Yu based on YLZB11691-A and YLZB11691-B specimens stored in CDBI.

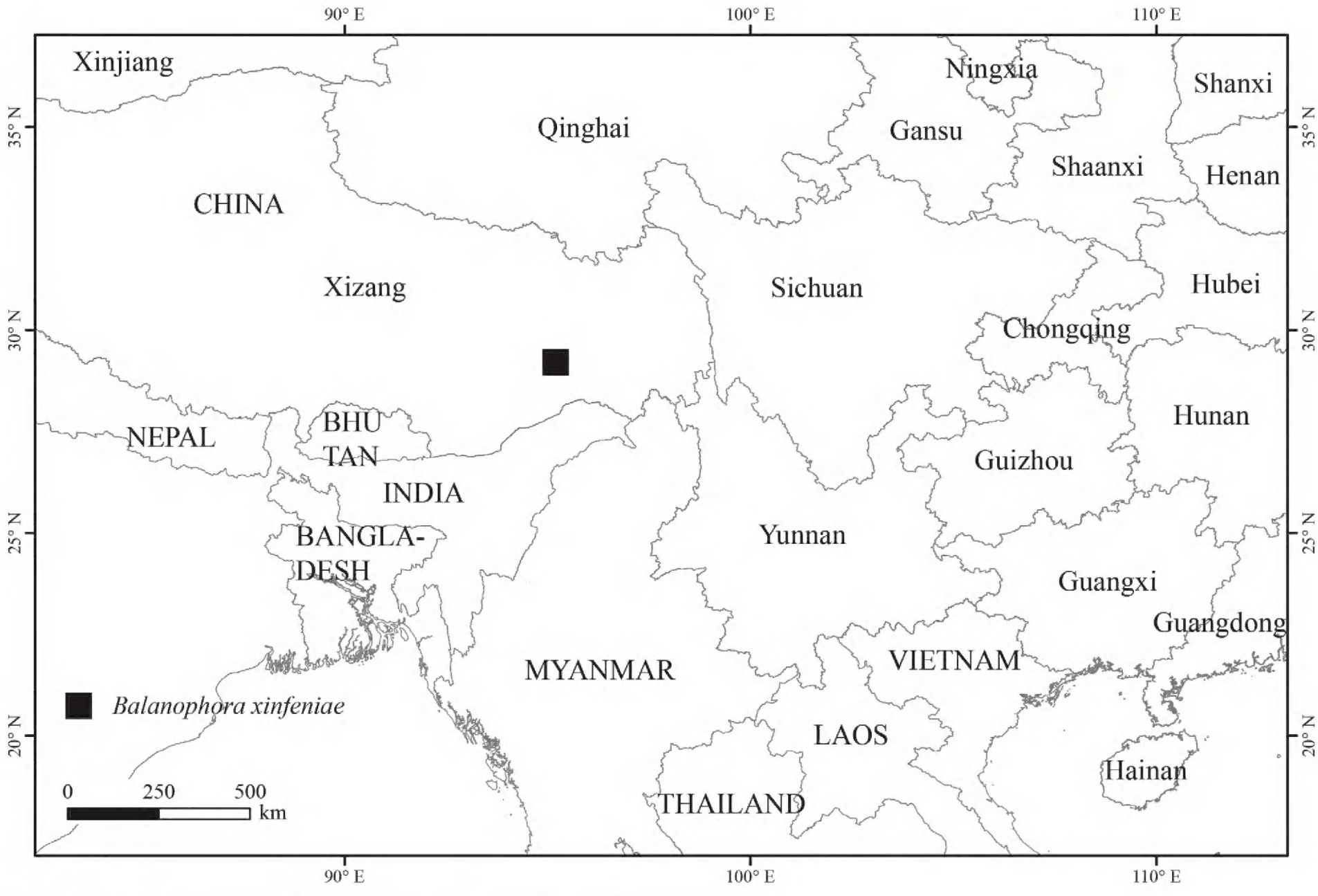


**Figure 5.** Distribution of *Balanophora xinfeniae* (Balanophoraceae).

**Phenology.** The species has been observed flowering from April to May.

**Etymology.** The species epithet *xinfeniae* honors Prof. Xin-Fen Gao (former curator of the CDBI Herbarium), a distinguished botanist who made significant contributions to the taxonomy of seed plants, lycopods, and pteridophytes.

**Vernacular name.** Chinese Mandarin: Xìn fēn shé gū (信芬蛇菰).

**Additional specimens examined.** China • Xizang Autonomous Region: Motuo County, Gelin Village, 29.210161°N, 95.191856°E, alt. 1650 m, 29 Apr 2024 (fl.), *Meng Li, C.L. Fu & J.N. Zhou YLZB11691-B* (paratype: CDBI! Barcode number: CDBI0298363, ♂; NAS! Barcode number: NAS00708510, ♂; NF!, ♂); • Gelin Village, 29.220615°N, 95.189094°E, alt. 1602 m, 1 May 2024 (fl.), *Meng Li MD2405013-B* (paratype: CDBI! Barcode number: CDBI0298362, ♂); • Gelin Village, alt. 1700 m, 24 May 1983 (fl.), *B.S. Li, S.Z. Cheng & Z.C. Nie 03761* (PE! Barcode number: PE01491372; PE01801408); • Beibeng Township, alt. 1650 m, 11 May 1983 (fl.), *S.Z. Cheng, Z.C. Nie & B.S. Li 04844* (PE! Barcode number: PE01491371).

### Key to the new species of *Balanophora* and three morphologically similar taxa

1 Leaves connate into a single sheath-like whorl.....**2**
– Leaves opposite .....**3**
2 Plants monoecious, male flowers clustered basally on inflorescence..... ..... ***Balanophora involucrata***
– Plants dioecious.....***Balanophora flava***
3 Scapes yellow, apical leaf margins prominently and irregularly serrate, female inflorescence nearly spherical or ovoid-ellipsoid .....***Balanophora xinfeniae***
– Scapes red or red to yellow, leaf margins entire, female inflorescence broadly ovoid ..... ***Balanophora henryi***

## Acknowledgements

We sincerely thank the reviewers and editors for their valuable comments. We are grateful to Prof. Yong Yang for his guidance on specimen preparation and to Xiao-Xia Ding and Xiao-Yu Dong for preparing the type specimens. We also thank Yan-Feng Song for assistance in examining the specimens stored in PE and extend special thanks to Zi-Heng Yu for drawing the line illustrations. We appreciate the support of the Forestry and Grassland Bureau of Linzhi City and the Forestry and Grassland Bureau of Motuo County for issuing the collection permits.

## Additional information

### Conflict of interest

The authors have declared that no competing interests exist.

### Ethical statement

No ethical statement was reported.

### Use of AI

No use of AI was reported.

## Funding

This study was funded by the Science and Technology Major Project of Xizang (XZ202501ZY05151) and the Second Tibetan Plateau Scientific Expedition and Research (STEP) Program (2024QZKK0200).

## Author contributions

B.X. and M.L. designed and led the project. C.F., J.Z. and M.L. collected the samples. C.F. performed data analyses and wrote the manuscript. W.L. and T.Z. provided the technical supports. M.L. revised the paper. All authors read and approved the final version of the manuscript.

## Author ORCIDs

Chen-Long Fu https://orcid.org/0000-0003-3752-461X
Jia-Ning Zhou https://orcid.org/0009-0005-4280-4706
Wei-Hua Liao https://orcid.org/0009-0004-3504-3155
Tong Zhang https://orcid.org/0009-0009-1492-585X
Bo Xu https://orcid.org/0000-0003-3507-9321
Meng Li https://orcid.org/0000-0003-2085-3388

## Data availability

All of the data that support the findings of this study are available in the main text or Supplementary Information.

## References

Chen XL, Fang DM, Xu YX, Duan K, Yoshida S, Yang S, Sahu SK, Fu H, Guang XM, Liu M, Wu CY, Liu Y, Mu WX, Chen YW, Fan YN, Wang F, Peng SF, Shi DS, Wang YY, Yu RX, Zhang W, Bai YQ, Liu ZJ, Yan QS, Liu X, Xu X, Yang HM, Wu JQ, Graham SW, Liu H (2023) *Balanophora* genomes display massively convergent evolution with other extreme holoparasites and provide novel insights into parasite–host interactions. Nature Plants 9: 1627–1642. https://doi.org/10.1038/s41477-023-01517-7

Darriba D, Taboada GL, Doallo R, Posada D (2012) jModelTest 2: more models, new heuristics and parallel computing. Nature Methods 9(8): 772. https://doi.org/10.1038/nmeth.2109

Geng ST (2016) Systematics of *Balanophora* subgenus *Balania* (Balanophoraceae). M.S. Thesis, National Taiwan University, China. https://doi.org/10.6342/NTU201601573

Hansen B (1972) The genus *Balanophora* J.R. & G. Forster. A taxonomic monograph. Dansk Botanisk Arkiv 28: 1–196.

Hsiao SC, Huang WT, Lin MS (2010) Genetic diversity of *Balanophora fungosa* and its conservation in Taiwan. Botanical Studies 51: 217–222.

Huang S, Murata J (2003) Balanophoraceae. Flora of China. Science Press, Beijing / Missouri Botanical Garden Press, St. Louis, 272–276.

Job K, Bertel H (2015) Santalales, Balanophorales. In: Flowering Plants. Eudicots. Springer International Publishing, Cham, 193–208. https://doi.org/10.1007/978-3-319-09296-6_23

Katoh K, Standley DM (2013) MAFFT multiple sequence alignment software version 7: improvements in performance and usability. Molecular Biology and Evolution 30(4): 772–780. https://doi.org/10.1093/molbev/mst010

Katoh K, Misawa K, Kuma KI, Miyata T (2002) MAFFT: a novel method for rapid multiple sequence alignment based on fast Fourier transform. Nucleic Acids Research 30(14): 3059–3066. https://doi.org/10.1093/nar/gkf436

Li SM, Long CL, Liu FY, Lee S, Guo Q, Li R, Liu YH (2006) Herbs for medicinal baths among the traditional Yao communities of China. Journal of Ethnopharmacology 108(1): 59–67. https://doi.org/10.1016/j.jep.2006.04.014

Lidén M (2019) Balanophoraceae, SE Asia: On the Identity of *Balanophora involucrata* Hook.f. and *B. flava* (Hook.f.) Lidén Comb. Nov. Pleione 13(1): 139–141. https://doi.org/10.26679/Pleione.13.1.2019.139-141

Minh BQ, Schmidt HA, Chernomor O, Schrempf D, Woodhams MD, von Haeseler A, Lanfear R (2020) IQ-TREE 2: new models and efficient methods for phylogenetic inference in the genomic era. Molecular Biology and Evolution 37(5): 1530–1534. https://doi.org/10.1093/molbev/msaa015

Mutinda ES, Zhang DJ, Muema FW, Mkala EM, Waswa EN, Odago WO, Onyango Ochieng C, Gichua MK, Muchuku JK, Kamande E, Hu GW (2024) The genus *Balanophora* J. R. Forst. & G. Forst. – Its use in traditional medicine, phytochemistry, and pharmacology: A review. Journal of Ethnopharmacology 319(3): 117276. https://doi.org/10.1016/j.jep.2023.117276

Rambaut A (2009) FigTree. Tree figure drawing tool. http://tree.bio.ed.ac.uk/software/figtree/

Ronquist F, Teslenko M, Mark P van der, Ayres DL, Darling A, Höhna S, Larget B, Liu L, Suchard MA, Huelsenbeck JP (2012) MrBayes 3.2: efficient Bayesian phylogenetic inference and model choice across a large model space. Systematic Biology 61(3): 539–542. https://doi.org/10.1093/sysbio/sys029

Sanchez-Puerta MV, Ceriotti LF, Gatica-Soria LM, Roulet ME, Garcia LE, Sato HA (2023) Beyond parasitic convergence: unravelling the evolution of the organellar genomes in holoparasites. Annals of Botany 132(5): 909–928. https://doi.org/10.1093/aob/mcad108

Su HJ, Murata J, Hu JM (2012) Morphology and phylogenetics of two holoparasitic plants, *Balanophora japonica* and *Balanophora yakushimensis* (Balanophoraceae), and their hosts in Taiwan and Japan. Journal of Plant Research 125: 317–326. https://doi.org/10.1007/s10265-011-0447-5

Su HJ, Barkman TJ, Hao W, Jones SS, Naumann J, Skippington E, Wafula EK, Hu JM, Palmer JD, dePamphilis CW (2019) Novel genetic code and record-setting AT-richness in the highly reduced plastid genome of the holoparasitic plant *Balanophora*. Proceedings of the National Academy of Sciences 116(3): 934–943. https://doi.org/10.1073/pnas.1816822116

Teng RW, Wang DZ, Yang CR (2000) Chemical constituents from *Balanophora harlandii*. Acta Botanica Yunnanica 22: 225–233.

Thiers BM (2024) Index Herbariorum. https://sweetgum.nybg.org/science/ih/

Trakulsomboon S, Kummalue T, Jiratchariyakul W (2006) Antibacterial activities of four Thai medicinal plants. 89(9): 1466–1471.

Yu RX, Zhou SY, Li YQ, Ma KN, Li YY, Huang LS, Zhou RC, Liu Y (2021) Two New Species of *Balanophora* (Balanophoraceae) From South China. Systematic Botany 46(4): 1053–1066. https://doi.org/10.1600/036364421X16370110179500

Yu RX, Zhou SY, Chen XL, Fang DM, Yue XY, Ma KN, Zhou RC, Liu Y (2022) Exploring the Species Limits in *Balanophora* subgenus *Balania*. Systematic Botany 47(3): 869–875. https://doi.org/10.1600/036364422X16573022073581

## Supplementary material 1

### Multiple-sequence alignment in FASTA format

Authors: Chen-Long Fu, Jia-Ning Zhou, Wei-Hua Liao, Tong Zhang, Bo Xu, Meng Li

Data type: fasta

Copyright notice: This dataset is made available under the Open Database License (http://opendatacommons.org/licenses/odbl/1.0/). The Open Database License (ODbL) is a license agreement intended to allow users to freely share, modify, and use this Dataset while maintaining this same freedom for others, provided that the original source and author(s) are credited.

Link: https://doi.org/10.3897/phytokeys.266.147400.suppl1

## Supplementary material 2

### Multiple-sequence alignment in NEX format

Authors: Chen-Long Fu, Jia-Ning Zhou, Wei-Hua Liao, Tong Zhang, Bo Xu, Meng Li

Data type: nex

Copyright notice: This dataset is made available under the Open Database License (http://opendatacommons.org/licenses/odbl/1.0/). The Open Database License (ODbL) is a license agreement intended to allow users to freely share, modify, and use this Dataset while maintaining this same freedom for others, provided that the original source and author(s) are credited.

Link: https://doi.org/10.3897/phytokeys.266.147400.suppl2